

**IN THE SPECIFICATION:**

Please amend the paragraph beginning on page 39, line 3 as follows:

Data analysis. The translated amino acid sequence of FAM was analyzed using the following INTERNET based software programs: Tmpred, FASTA, ScanProsite, PfamHMM, PSORT, SSPRED, ProfileScan, ProtScale, PatScan, pI/Mw, and Motif (available through Pedro's BioMolecular Research Tools at [http://www.public.iastate.edu/~pedro/rtz\\_1.html](http://www.public.iastate.edu/~pedro/rtz_1.html)), SignalP (<http://www.cbs.dtu.dk/services/SignalP/output.html>), Pfam (The Sanger Centre, <http://www.sanger.ac.uk>) and Simple Modular Architecture Research Tool ([http://coot.embl-heidelberg.de/predict\\_protein](http://coot.embl-heidelberg.de/predict_protein)).